



## SEQUENCE LISTING

<110> Fukuda, Atsunori  
Tanaka, Yoshiyuki

<120> Sodium/Proton Antiporter Gene

<130> SPO-115C1

<140> 09/888,035

<141> 2001-06-22

<150> JP 1998-365604

<151> 1998-12-22

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<170> PatentIn version 3.1

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tctgcgaatc gaattctttg tttttttttc tctaatttta ccgggaattg tcgaattagg 180  
cattcaccaa cgagcaagag gggagtggtat tggttgggta aagctccgca tcttgcgggc 240  
gaaatctcgc tctcttctct gcggtgggtg gccggagaag tcgccgccgg tgaggc atg 299  
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ggg atg gag gtg gcg gcg gcg cgg ctg ggg gct ctg tac acg acc tcc 347  
Gly Met Glu Val Ala Ala Ala Arg Leu Gly Ala Leu Tyr Thr Thr Ser  
5 10 15

gac tac gcg tcg gtg gtg tcc atc aac ctg ttc gtc gcg ctg ctc tgc 395  
Asp Tyr Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Leu Cys  
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gcc tgc atc gtc ctc ggc cac ctc ctc gag gag aat cgc tgg gtc aat Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val Asn 35 40 45	443
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ttg ctg atg acc aaa ggg aag agc tcg cac tta ttc gtc ttc agt gag Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser Glu 70 75 80	539
gat ctc ttc ttc atc tac ctc ctc cct ccg atc atc ttc aat gca ggt Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly 85 90 95	587
ttt cag gta aag aaa aag caa ttc ttc cgg aat ttc atg acg atc aca Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile Thr 100 105 110	635
tta ttt gga gcc gtc ggg aca atg ata tcc ttt ttc aca ata tct att Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser Ile 115 120 125	683
gct gcc att gca ata ttc agc aga atg aac att gga acg ctg gat gta Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp Val 130 135 140 145	731
gga gat ttt ctt gca att gga gcc atc ttt tct gcg aca gat tct gtc Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser Val 150 155 160	779
tgc aca ttg cag gtc ctc aat cag gat gag aca ccc ttt ttg tac agt Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Phe Leu Tyr Ser 165 170 175	827
ctg gta ttc ggt gaa ggt gtt gtg aac gat gct aca tca att gtg ctt Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val Leu 180 185 190	875
ttc aac gca cta cag aac ttt gat ctt gtc cac ata gat gcg gct gtc Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala Val 195 200 205	923
gtt ctg aaa ttc ttg ggg aac ttc ttt tat tta ttt ttg tcg agc acc Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser Thr 210 215 220 225	971
ttc ctt gga gta ttt gct gga ttg ctc agt gca tac ata atc aag aag Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys Lys 230 235 240	1019

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ggc att ctc acc gta ttc ttc tgt ggt att gta atg tca cat tac act Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr 275 280 285	1163
tgg cat aac gtc aca gag agt tca aga gtt aca aca aag cac gca ttt Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala Phe 290 295 300 305	1211
gca act ctg tcc ttc att gct gag act ttt ctc ttc ctg tat gtt ggg Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val Gly 310 315 320	1259
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His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser Pro  
450 455 460 465  
  
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Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn Ile  
470 475 480  
  
gtg agg cct tcc agc ctc cgg atg ctc ctc acc aag ccg acc cac act 1787  
Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His Thr  
485 490 495  
  
gtc cac tac tac tgg cgc aag ttc gac gac gcg ctg atg cga ccg atg 1835  
Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro Met  
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Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr Glu  
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Gln Ser His Gly Gly Arg  
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 35 40 45

Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val  
 50 55 60

Ile Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser  
 65 70 75 80

Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala  
 85 90 95

Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile  
 100 105 110

Thr Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser  
 115 120 125

Ile Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp  
 130 135 140

Val Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser  
 145 150 155 160

Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Phe Leu Tyr  
 165 170 175

Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val  
 180 185 190

Leu Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala  
 195 200 205

Val Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser  
 210 215 220

Thr Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys  
 225 230 235 240

Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met  
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Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu  
260 265 270

Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr  
275 280 285

Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala  
290 295 300

Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val  
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Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg  
325 330 335

Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu  
340 345 350

Ile Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu  
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Thr Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val  
370 375 380

Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala  
385 390 395 400

Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala  
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Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val  
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Phe Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser  
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Gly His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser  
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Pro Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn  
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Ile Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His  
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Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro  
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Met Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr  
515 520 525

Glu Gln Ser His Gly Gly Arg  
530 535